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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/543,371A

DATE: 09/26/2002
TIME: 16:28:03

Input Set : A:\09543371.ST25.txt
Output Set: N:\CRF4\09262002\I543371A.raw

3 <110> APPLICANT: Kalluri, Raghuram
5 <120> TITLE OF INVENTION: Anti-Angiogenic Proteins and Fragments and Methods of Use
Thereof

7 <130> FILE REFERENCE: 02312/2085B (formerly 1440.1027-005)

9 <140> CURRENT APPLICATION NUMBER: US 09/543,371A

10 <141> CURRENT FILING DATE: 2000-04-04

12 <150> PRIOR APPLICATION NUMBER: US 60/089,689

13 <151> PRIOR FILING DATE: 1998-06-17

15 <150> PRIOR APPLICATION NUMBER: US 60/126,175

16 <151> PRIOR FILING DATE: 1999-03-25

18 <150> PRIOR APPLICATION NUMBER: US 09/335,224

19 <151> PRIOR FILING DATE: 1999-06-17

21 <160> NUMBER OF SEQ ID NOS: 18

23 <170> SOFTWARE: PatentIn version 3.1

25 <210> SEQ ID NO: 1

26 <211> LENGTH: 690

27 <212> TYPE: DNA

28 <213> ORGANISM: Homo sapiens

30 <220> FEATURE:

31 <221> NAME/KEY: CDS

32 <222> LOCATION: (1)..(687)

33 <223> OTHER INFORMATION:

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37 Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile Asp

38 1 5 10 15

40 gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac tct 96

41 Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr Ser

42 20 25 30

44 ttg ctc tac gtg caa ggc aat gaa cgg gcc cat gga cag gac ttg ggc 144

45 Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu Gly

46 35 40 45

48 acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg ttc 192

49 Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu Phe

50 50 55 60

52 tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac tcg 240

53 Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr Ser

54 65 70 75 80

56 tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc atc 288

57 Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro Ile

58 85 90 95

60 acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt gag 336

61 Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys Glu

62 100 105 110

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64	gcg	cct	gcc	atg	gtg	atg	gcc	gtg	cac	agc	cag	acc	att	cag	atc	cca	384
65	Ala	Pro	Ala	Met	Val	Met	Ala	Val	His	Ser	Gln	Thr	Ile	Gln	Ile	Pro	
66				115				120						125			
68	ccg	tgc	ccc	agc	ggg	tgg	tcc	tcg	ctg	tgg	atc	gcc	tac	tct	ttt	gtg	432
69	Pro	Cys	Pro	Ser	Gly	Trp	Ser	Ser	Leu	Trp	Ile	Gly	Tyr	Ser	Phe	Val	
70				130				135				140					
72	atg	cac	acc	agc	gct	ggt	gca	gaa	ggc	tct	ggc	caa	gcc	ctg	gcg	tcc	480
73	Met	His	Thr	Ser	Ala	Gly	Ala	Glu	Gly	Ser	Gly	Gln	Ala	Leu	Ala	Ser	
74	145				150						155			160			
76	ccc	ggc	tcc	tgc	ctg	gag	gag	ttt	aga	agt	gcg	cca	ttc	atc	gag	tgt	528
77	Pro	Gly	Ser	Cys	Leu	Glu	Glu	Phe	Arg	Ser	Ala	Pro	Phe	Ile	Glu	Cys	
78					165				170			175					
80	cac	ggc	cgt	ggg	acc	tgc	aat	tac	tac	gca	aac	gct	tac	agc	ttt	tgg	576
81	His	Gly	Arg	Gly	Thr	Cys	Asn	Tyr	Tyr	Ala	Asn	Ala	Tyr	Ser	Phe	Trp	
82					180				185			190					
84	ctc	gcc	acc	ata	gag	agg	agc	gag	atg	ttc	aag	aag	cct	acg	ccg	tcc	624
85	Leu	Ala	Thr	Ile	Glu	Arg	Ser	Glu	Met	Phe	Lys	Lys	Pro	Thr	Pro	Ser	
86				195				200			205						
88	acc	ttg	aag	gca	ggg	gag	ctg	cgc	acg	cac	gtc	agc	cgc	tgc	caa	gtc	672
89	Thr	Leu	Lys	Ala	Gly	Glu	Leu	Arg	Thr	His	Val	Ser	Arg	Cys	Gln	Val	
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108	Asp	Pro	Gln	Cys	Pro	Ser	Gly	Thr	Lys	Ile	Leu	Tyr	His	Gly	Tyr	Ser	
109					20				25			30					
112	Leu	Leu	Tyr	Val	Gln	Gly	Asn	Glu	Arg	Ala	His	Gly	Gln	Asp	Leu	Gly	
113					35				40			45					
116	Thr	Ala	Gly	Ser	Cys	Leu	Arg	Lys	Phe	Ser	Thr	Met	Pro	Phe	Leu	Phe	
117					50				55			60					
120	Cys	Asn	Ile	Asn	Asn	Val	Cys	Asn	Phe	Ala	Ser	Arg	Asn	Asp	Tyr	Ser	
121	65					70				75			80				
124	Tyr	Trp	Leu	Ser	Thr	Pro	Glu	Pro	Met	Pro	Met	Ser	Met	Ala	Pro	Ile	
125					85				90			95					
128	Thr	Gly	Glu	Asn	Ile	Arg	Pro	Phe	Ile	Ser	Arg	Cys	Ala	Val	Cys	Glu	
129					100				105			110					
132	Ala	Pro	Ala	Met	Val	Met	Ala	Val	His	Ser	Gln	Thr	Ile	Gln	Ile	Pro	
133					115				120			125					
136	Pro	Cys	Pro	Ser	Gly	Trp	Ser	Ser	Leu	Trp	Ile	Gly	Tyr	Ser	Phe	Val	
137					130				135			140					
140	Met	His	Thr	Ser	Ala	Gly	Ala	Glu	Gly	Ser	Gly	Gln	Ala	Leu	Ala	Ser	
141	145					150					155			160			

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144 Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu Cys
 145 165 170 175
 148 His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe Trp
 149 180 185 190
 152 Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro Ser
 153 195 200 205
 156 Thr Leu Lys Ala Gly Glu Leu Arg Thr His Val Ser Arg Cys Gln Val
 157 210 215 220
 160 Cys Met Arg Arg Thr
 161 225
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 165 <211> LENGTH: 27
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 167 <213> ORGANISM: Artificial sequence
 169 <220> FEATURE:
 170 <223> OTHER INFORMATION: pET22b(+) forward oligonucleotide primer for Arresten
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 178 <212> TYPE: DNA
 179 <213> ORGANISM: Artificial sequence
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 185 cccaaagcttt gttcttctca tacagac 27
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 189 <211> LENGTH: 684
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 194 <221> NAME/KEY: CDS
 195 <222> LOCATION: (1)..(681)
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 200 Val Ser Ile Gly Tyr Leu Leu Val Lys His Ser Gln Thr Asp Gln Glu
 201 1 5 10 15
 203 ccc atg tgc cgc gtg ggc atg aac aaa ctc tgg agt gga tac agc ctg 96
 204 Pro Met Cys Pro Val Gly Met Asn Lys Leu Trp Ser Gly Tyr Ser Leu
 205 20 25 30
 207 ctg tac ttc gag ggc cag gag aag gcg cac aac cag gac ctg ggg ctg 144
 208 Leu Tyr Phe Glu Gly Gln Glu Lys Ala His Asn Gln Asp Leu Gly Leu
 209 35 40 45
 211 gcg ggc tcc tgc ctg gcg cgg ttc agc acc atg ccc ttc ctg tac tgc 192
 212 Ala Gly Ser Cys Leu Ala Arg Phe Ser Thr Met Pro Phe Leu Tyr Cys
 213 50 55 60
 215 aac cct ggt gat gtc tgc tac tat gcc agc cgg aac gac aag tcc tac 240
 216 Asn Pro Gly Asp Val Cys Tyr Tyr Ala Ser Arg Asn Asp Lys Ser Tyr

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220	Trp	Leu	Ser	Thr	Thr	Ala	Pro	Leu	Pro	Met	Met	Pro	Val	Ala	Glu	Asp	
221																95	
223	gag	atc	aag	ccc	tac	atc	agc	cgc	tgt	tct	gtg	tgt	gag	gcc	ccg	gcc	336
224	Glu	Ile	Lys	Pro	Tyr	Ile	Ser	Arg	Cys	Ser	Val	Cys	Glu	Ala	Pro	Ala	
225																110	
227	atc	gcc	atc	gcf	gtc	cac	agt	cag	gat	gtc	tcc	atc	cca	cac	tgc	cca	384
228	Ile	Ala	Ile	Ala	Val	His	Ser	Gln	Asp	Val	Ser	Ile	Pro	His	Cys	Pro	
229																125	
231	gct	ggg	tgg	cgf	agt	ttg	tgg	atc	gga	tat	tcc	ttc	ctc	atg	cac	acg	432
232	Ala	Gly	Trp	Arg	Ser	Leu	Trp	Ile	Gly	Tyr	Ser	Phe	Leu	Met	His	Thr	
233																140	
235	gcf	gcf	gga	gac	gaa	ggc	ggt	ggc	caa	tca	ctg	gtg	tca	ccg	ggc	agc	480
236	Ala	Ala	Gly	Asp	Glu	Gly	Gly	Gly	Gln	Ser	Leu	Val	Ser	Pro	Gly	Ser	
237																160	
239	tgt	cta	gag	gac	ttc	cgf	gcc	aca	cca	ttc	atc	gaa	tgc	aat	gga	ggc	528
240	Cys	Leu	Glu	Asp	Phe	Arg	Ala	Thr	Pro	Phe	Ile	Glu	Cys	Asn	Gly	Gly	
241																175	
243	cgf	ggc	acc	tgc	cac	tac	tac	gcc	aac	aag	tac	agc	ttc	tgg	ctg	acc	576
244	Arg	Gly	Thr	Cys	His	Tyr	Tyr	Ala	Asn	Lys	Tyr	Ser	Phe	Trp	Leu	Thr	
245																190	
247	acc	att	ccc	gag	cag	agc	ttc	cag	ggc	tcg	ccc	tcc	gcc	gac	acg	ctc	624
248	Thr	Ile	Pro	Glu	Gln	Ser	Phe	Gln	Gly	Ser	Pro	Ser	Ala	Asp	Thr	Leu	
249																205	
251	aag	gcc	ggc	ctc	atc	cgf	aca	cac	atc	agc	cgf	tgc	cag	gtg	tgc	atg	672
252	Lys	Ala	Gly	Leu	Ile	Arg	Thr	His	Ile	Ser	Arg	Cys	Gln	Val	Cys	Met	
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271	Pro	Met	Cys	Pro	Val	Gly	Met	Asn	Lys	Leu	Trp	Ser	Gly	Tyr	Ser	Leu	
272							20			25			30				
275	Leu	Tyr	Phe	Glu	Gly	Gln	Glu	Lys	Ala	His	Asn	Gln	Asp	Leu	Gly	Leu	
276							35			40			45				
279	Ala	Gly	Ser	Cys	Leu	Ala	Arg	Phe	Ser	Thr	Met	Pro	Phe	Leu	Tyr	Cys	
280							50			55			60				
283	Asn	Pro	Gly	Asp	Val	Cys	Tyr	Tyr	Ala	Ser	Arg	Asn	Asp	Lys	Ser	Tyr	
284	65						70				75			80			
287	Trp	Leu	Ser	Thr	Thr	Ala	Pro	Leu	Pro	Met	Met	Pro	Val	Ala	Glu	Asp	
288										85			90			95	
291	Glu	Ile	Lys	Pro	Tyr	Ile	Ser	Arg	Cys	Ser	Val	Cys	Glu	Ala	Pro	Ala	

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292 100 105 110
 295 Ile Ala Ile Ala Val His Ser Gln Asp Val Ser Ile Pro His Cys Pro
 296 115 120 125
 299 Ala Gly Trp Arg Ser Leu Trp Ile Gly Tyr Ser Phe Leu Met His Thr
 300 130 135 140
 303 Ala Ala Gly Asp Glu Gly Gly Gln Ser Leu Val Ser Pro Gly Ser
 304 145 150 155 160
 307 Cys Leu Glu Asp Phe Arg Ala Thr Pro Phe Ile Glu Cys Asn Gly Gly
 308 165 170 175
 311 Arg Gly Thr Cys His Tyr Tyr Ala Asn Lys Tyr Ser Phe Trp Leu Thr
 312 180 185 190
 315 Thr Ile Pro Glu Gln Ser Phe Gln Gly Ser Pro Ser Ala Asp Thr Leu
 316 195 200 205
 319 Lys Ala Gly Leu Ile Arg Thr His Ile Ser Arg Cys Gln Val Cys Met
 320 210 215 220
 323 Lys Asn Leu
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 336 cgggatcctg tcagcatcg 27
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 342 <213> ORGANISM: Artificial sequence
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 351 <210> SEQ ID NO: 9
 352 <211> LENGTH: 735
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 363 <222> LOCATION: (160)..(732)
 364 <223> OTHER INFORMATION: Tumstatin N53
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 369 <222> LOCATION: (1)..(372)
 370 <223> OTHER INFORMATION: Tumstatin 333

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/543,371A

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